R. Mitra

9
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/687,276

DATE: 09/06/2001
TIME: 10:55:17

Input Set : A:\Cura-851.app
Output Set: N:\CRF3\09062001\I687276.raw

ENTERED

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 3 <110> APPLICANT: Prayaga, Sudhirdas K
 4         Taupier Jr, Raymond J
 5         Bandaru, Raj
 7 <120> TITLE OF INVENTION: NOVEL THYMOSIN BETA 10-LIKE PROTEINS AND NUCLEIC ACIDS
 8         ENCODING SAME
10 <130> FILE REFERENCE: 15966-585A
12 <140> CURRENT APPLICATION NUMBER: 09/687,276
13 <141> CURRENT FILING DATE: 2000-10-13
15 <150> PRIOR APPLICATION NUMBER: 60/159,805
16 <151> PRIOR FILING DATE: 1999-10-15
18 <150> PRIOR APPLICATION NUMBER: 60/159,992
19 <151> PRIOR FILING DATE: 1999-10-18
21 <150> PRIOR APPLICATION NUMBER: 60/160,952
22 <151> PRIOR FILING DATE: 1999-10-22
24 <160> NUMBER OF SEQ ID NOS: 64
26 <170> SOFTWARE: PatentIn Ver. 2.1
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30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
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41 Met Ala Asp Lys Pro Asp Ile Gly Glu Ile Ala Ser Phe Asn Lys Ala
42   1               5                  10                  15
44 aag ctg aag aaa aca gag atg cag gag aac acc ctg ctg acc aaa gag    156
45 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
46           20                  25                  30
48 gcc att gag cag gag aag cgg gtg aaa ttt cct aag agc ctg gag gat    204
49 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
50           35                  40                  45
52 tcc cta ccc ctg tca tct tcg aga ccc cag tagtaatgtg gaggaagaat    254
53 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
54        50                  55
56 caccacaaga tggacacaag ccacaaactg tgacgtgaac ctgggcactc cgtgctgatg 314
58 ccaccagcct gagggtccct atgggtccaa tcagactgcc aaattctctg gtttgccctg 374
60 ggatattata gaaaattatt tgcgtgaata atgaaaacac agctcatggc aaaaaa    430
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 58
65 <212> TYPE: PRT
66 <213> ORGANISM: Homo sapiens
68 <400> SEQUENCE: 2
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70   1               5                  10                  15
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72 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
73              20                  25                  30
75 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
76          35                  40                  45
78 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
79       50                  55
83 <210> SEQ ID NO: 3
84 <211> LENGTH: 13
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 3
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101 cacggggact ggggctggct cacgtatccg gctcatgggt gggactccat caacgaggtg 180
102 gacgagtcct tccagcccat ccacacgtac caggtttgca acgtcatgag ccccaaccag 240
103 aacaactggc tgcgcacgag ctgggtcccc cgagacggcg cccggcgcgt ctatgctgag 300
104 atcaagttta ccctgcgcga ctgcaacagc atgcctggtg tgctgggcac ctgcaaggag 360
105 accttcaacc tctactacct ggagtcggac cgcgacctgg gggccagcac acaagaaagc 420
106 cagttcctca aaatcgacac cattgcggcc gacgagagct tcacaggtgc cgaccttggt 480
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109 tataagaagt gccctgccat ggtgcgcaat ctggctgcct tctcggaggc agtgacgggg 660
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111 gacacaccca agatgtactg cagcgcggag ggcgagtggc tcgtgcccat cggcaaatgc 780
112 gtgtgcagtg ccggctacga ggagcggcgg gatgcctgtg tggcctgtga gctgggcttc 840
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114 gctccagccg cccaagcctg ccactgtgac ctcagctact accgtgcagc cctggacccg 960
115 ccgtcctcag cctgcacccg gccaccctcg gcaccagtga acctgatctc cagtgtgaat 1020
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117 acctacaatg ccgtgtgccg ccgctgcccc tgggcactga ccgctgcga ggcatgtggg 1140
118 agcggcaccc gctttgtgcc ccagcagaca agcctggtgc aggccagcct gctggtggcc 1200
119 aacctgctgg cccacatgaa ctactccttc tggatcgagg ccgtcaatgg cgtgtccgac 1260
120 ctgagccccg agccccgccg ggccgctgtg gtcaacatca ccacgaacca ggcagccccg 1320
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123 gacaaggaga tgcagagcta ctccaccctc aaggccgtca ccaccagagc caccgtctcc 1500
124 ggcctcaagc cgggcacccg ctacgtgttc caggtccgag cccgcacctc agcaggctgt 1560
125 ggccgcttca gccaggccat ggaggtggag accgggaaac cccggccccg ctatgacacc 1620
126 aggaccattg tctggatctg cctgacgctc atcacgggcc tggtggtgct tctgctcctg 1680
127 ctcatctgca gaagaggca ctgtggctac agcaaggcct tccaggactc ggacgaggag 1740
128 aagatgcact atcagaatgg acaggcaccc ccacctgtct tcctgcctct gcatcacccc 1800
129 ccgggaaagc tcccagagcc ccagttctat gcggaacccc acacctacga ggagccaggc 1860
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Output Set: **N:\CRF3\09062001\I687276.raw**

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131 atcggctctg gagactccgg ggaagtctgc tacgggaggc tgcgggtgcc agggcagcgg 1980
132 gatgtgcccg tggccatcaa ggccctcaaa gccggctaca cggagagaca gaggcgggac 2040
133 ttcctgagcg aggcgtccat catggggcaa ttcgaccatc ccaacatcat ccgcctcgag 2100
134 ggtgtcgtca cccgtggccg cctggcaatg attgtgactg agtacatgga gaacggctct 2160
135 ctggacacct tcctgaggac ccacgacggg cagttcacca tcatgcagct ggtgggcatg 2220
136 ctgagaggag tgggtgccgg catgcgctac ctctcagacc tgggctatgt ccaccgagac 2280
137 ctggccgccc gcaacgtcct ggttgacagc aacctggtct gcaaggtgtc tgacttcggg 2340
138 ctctcacggg tgctggagga cgacccggat gctgcctaca ccaccacggg cgggaagatc 2400
139 cccatccgct ggacggcccc agaggccatc gccttccgca ccttctcctc ggccagcgac 2460
140 gtgtggagct tcggcgtggt catgtgggag gtgctggcct atggggagcg gccctactgg 2520
141 aacatgacca accgggatgt gatcagctct gtggaggagg ggtaccgcct gcccgcaccc 2580
142 atgggctgcc cccacgccct gcaccagctc atgctcgact gttggcacaa ggaccgggcg 2640
143 cagcggcctc gcttctccca gattgtcagt gtcctcgatg cgctcatccg cagccctgag 2700
144 agtctcaggg ccaccgccac agtcagcagg tgcccacccc ctgccttcgt ccggagctgc 2760
145 tttgacctcc gaggggggcag cggtggcggt gggggcctca ccgtggggga ctggctggac 2820
146 tccatccgca tgggccggta ccgagaccac ttcgctgcgg gcggatactc ctctctgggc 2880
147 atggtgctac gcatgaacgc ccaggacgtg cgcgccctgg gcatcaccct catgggccac 2940
148 cagaagaaga tcctgggcag cattcagacc atgcgggccc agctgaccag cacccagggg 3000
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153 <211> LENGTH: 992
154 <212> TYPE: PRT
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157 <400> SEQUENCE: 5
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162             20                  25                  30
164 Asn Leu Leu Asp Thr Ser Thr Ile His Gly Asp Trp Gly Trp Leu Thr
165          35                  40                  45
167 Tyr Pro Ala His Gly Trp Asp Ser Ile Asn Glu Val Asp Glu Ser Phe
168       50                  55                  60
170 Gln Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Ser Pro Asn Gln
171  65                  70                  75                  80
173 Asn Asn Trp Leu Arg Thr Ser Trp Val Pro Arg Asp Gly Ala Arg Arg
174             85                  90                  95
176 Val Tyr Ala Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Met Pro
177             100                 105                 110
179 Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Leu Glu
180          115                 120                 125
182 Ser Asp Arg Asp Leu Gly Ala Ser Thr Gln Glu Ser Gln Phe Leu Lys
183       130                 135                 140
185 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gly Ala Asp Leu Gly
186 145                 150                 155                 160
188 Val Arg Arg Leu Lys Leu Asn Thr Glu Val Arg Ser Val Gly Pro Leu
189             165                 170                 175
191 Ser Lys Arg Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Leu
192             180                 185                 190
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194 Ala Ile Leu Ser Leu Arg Ile Tyr Tyr Lys Lys Cys Pro Ala Met Val
195         195             200         205
197 Arg Asn Leu Ala Ala Phe Ser Glu Ala Val Thr Gly Ala Asp Ser Ser
198     210             215             220
200 Ser Leu Val Glu Val Arg Gly Gln Cys Val Arg His Ser Glu Glu Arg
201 225             230             235             240
203 Asp Thr Pro Lys Met Tyr Cys Ser Ala Glu Gly Glu Trp Leu Val Pro
204             245             250             255
206 Ile Gly Lys Cys Val Cys Ser Ala Gly Tyr Glu Glu Arg Arg Asp Ala
207         260             265         270
209 Cys Val Ala Cys Glu Leu Gly Phe Tyr Lys Ser Ala Pro Gly Asp Gln
210     275             280             285
212 Leu Cys Ala Arg Cys Pro Pro His Ser His Ser Ala Ala Pro Ala Ala
213     290             295             300
215 Gln Ala Cys His Cys Asp Leu Ser Tyr Tyr Arg Ala Ala Leu Asp Pro
216 305             310             315             320
218 Pro Ser Ser Ala Cys Thr Arg Pro Pro Ser Ala Pro Val Asn Leu Ile
219             325             330             335
221 Ser Ser Val Asn Gly Thr Ser Val Thr Leu Glu Trp Ala Pro Pro Leu
222         340             345             350
224 Asp Pro Gly Gly Arg Ser Asp Ile Thr Tyr Asn Ala Val Cys Arg Arg
225         355             360             365
227 Cys Pro Trp Ala Leu Ser Arg Cys Glu Ala Cys Gly Ser Gly Thr Arg
228     370             375             380
230 Phe Val Pro Gln Gln Thr Ser Leu Val Gln Ala Ser Leu Leu Val Ala
231 385             390             395             400
233 Asn Leu Leu Ala His Met Asn Tyr Ser Phe Trp Ile Glu Ala Val Asn
234             405             410             415
236 Gly Val Ser Asp Leu Ser Pro Glu Pro Arg Arg Ala Ala Val Val Asn
237         420             425             430
239 Ile Thr Thr Asn Gln Ala Ala Pro Ser Gln Val Val Val Ile Arg Gln
240     435             440             445
242 Glu Arg Ala Gly Gln Thr Ser Val Ser Leu Leu Trp Gln Glu Pro Glu
243     450             455             460
245 Gln Pro Asn Gly Ile Ile Leu Glu Tyr Glu Ile Lys Tyr Tyr Glu Lys
246 465             470             475             480
248 Asp Lys Glu Met Gln Ser Tyr Ser Thr Leu Lys Ala Val Thr Thr Arg
249             485             490             495
251 Ala Thr Val Ser Gly Leu Lys Pro Gly Thr Arg Tyr Val Phe Gln Val
252         500             505             510
254 Arg Ala Arg Thr Ser Ala Gly Cys Gly Arg Phe Ser Gln Ala Met Glu
255     515             520             525
257 Val Glu Thr Gly Lys Pro Arg Pro Arg Tyr Asp Thr Arg Thr Ile Val
258     530             535             540
260 Trp Ile Cys Leu Thr Leu Ile Thr Gly Leu Val Val Leu Leu Leu Leu
261 545             550             555             560
263 Leu Ile Cys Lys Lys Arg His Cys Gly Tyr Ser Lys Ala Phe Gln Asp
264             565             570             575
266 Ser Asp Glu Glu Lys Met His Tyr Gln Asn Gly Gln Ala Pro Pro Pro
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267              580                 585                590
269  Val Phe Leu Pro Leu His His Pro Pro Gly Lys Leu Pro Glu Pro Gln
270          595                 600                605
272  Phe Tyr Ala Glu Pro His Thr Tyr Glu Glu Pro Gly Arg Ala Gly Arg
273      610                 615                620
275  Ser Phe Thr Arg Glu Ile Glu Ala Ser Arg Ile His Ile Glu Lys Ile
276  625                 630                635                640
278  Ile Gly Ser Gly Asp Ser Gly Glu Val Cys Tyr Gly Arg Leu Arg Val
279          645                 650                655
281  Pro Gly Gln Arg Asp Val Pro Val Ala Ile Lys Ala Leu Lys Ala Gly
282          660                 665                670
284  Tyr Thr Glu Arg Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met
285          675                 680                685
287  Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr
288      690                 695                700
290  Arg Gly Arg Leu Ala Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser
291  705                 710                715                720
293  Leu Asp Thr Phe Leu Arg Thr His Asp Gly Gln Phe Thr Ile Met Gln
294              725                 730                735
296  Leu Val Gly Met Leu Arg Gly Val Gly Ala Gly Met Arg Tyr Leu Ser
297          740                 745                750
299  Asp Leu Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
300          755                 760                765
302  Asp Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val
303      770                 775                780
305  Leu Glu Asp Asp Pro Asp Ala Ala Tyr Thr Thr Thr Gly Gly Lys Ile
306  785                 790                795                800
308  Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Thr Phe Ser
309              805                 810                815
311  Ser Ala Ser Asp Val Trp Ser Phe Gly Val Val Met Trp Glu Val Leu
312          820                 825                830
314  Ala Tyr Gly Glu Arg Pro Tyr Trp Asn Met Thr Asn Arg Asp Val Ile
315          835                 840                845
317  Ser Ser Val Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Gly Cys Pro
318      850                 855                860
320  His Ala Leu His Gln Leu Met Leu Asp Cys Trp His Lys Asp Arg Ala
321  865                 870                875                880
323  Gln Arg Pro Arg Phe Ser Gln Ile Val Ser Val Leu Asp Ala Leu Ile
324              885                 890                895
326  Arg Ser Pro Glu Ser Leu Arg Ala Thr Ala Thr Val Ser Arg Cys Pro
327          900                 905                910
329  Pro Pro Ala Phe Val Arg Ser Cys Phe Asp Leu Arg Gly Gly Ser Gly
330          915                 920                925
332  Gly Gly Gly Gly Leu Thr Val Gly Asp Trp Leu Asp Ser Ile Arg Met
333      930                 935                940
335  Gly Arg Tyr Arg Asp His Phe Ala Ala Gly Gly Tyr Ser Ser Leu Gly
336  945                 950                955                960
338  Met Val Leu Arg Met Asn Ala Gln Asp Val Arg Ala Leu Gly Ile Thr
339              965                 970                975
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VERIFICATION SUMMARY
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